

Multilevel analysis

Executive Functions in Primary Progressive Aphasia: a Meta-Analysis

Load packages

```
# devtools::install_github('MathiasHarrer/dmetar') install.packages('misty')
library(metafor)
library(ggplot2)
library(dmetar)
library(readxl)
library(formatR) # Rmarkdown text wrapping
library(misty) # Center variables
library(writexl)
library(FSA)
```

Importing data saved in an excel file

```
dat <- read_excel("~/Desktop/PhD/Review Neuropsych/Werk/Tabel_EF.xlsx", col_types = c("numeric",
"numeric", "numeric", "text", "numeric", "text", "text", "text", "text", "text",
"text", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric",
"numeric", "numeric", "numeric", "numeric", "numeric", "numeric", "numeric",
"numeric", "numeric", "text", "text"))
```

`read_excel("~/Desktop/PhD/Review Neuropsych/Werk/Tabel_EF.xlsx")` “Desktop/PhD/Review Neuropsych/Werk/Tabel_EF.xlsx” # Request an overview of the data structure and calculate effect sizes

```
str(dat)
dat <- escalc(measure = "SMD", m1i = m1i, sd1i = sd1i, n1i = n1i, m2i = m2i, sd2i = sd2i,
n2i = n2i, data = dat)
View(dat)
```

```
kruskal.test(m_patient_age ~ factor(variant, levels = c("LV", "SV", "NF")), data = dat)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: m_patient_age by factor(variant, levels = c("LV", "SV", "NF"))
## Kruskal-Wallis chi-squared = 55.944, df = 2, p-value = 7.11e-13
```

```
kruskal.test(m_disease_duration ~ factor(variant, levels = c("LV", "SV", "NF")),
  data = dat)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: m_disease_duration by factor(variant, levels = c("LV", "SV", "NF"))
## Kruskal-Wallis chi-squared = 31.402, df = 2, p-value = 1.518e-07
```

```
dunnTest(m_patient_age ~ factor(variant, levels = c("LV", "SV", "NF")), data = dat,
  method = "bh")
```

##	Comparison	Z	P.unadj	P.adj
## 1	LV - NF	-2.696146	7.014699e-03	7.014699e-03
## 2	LV - SV	2.826031	4.712865e-03	7.069298e-03
## 3	NF - SV	7.438975	1.014694e-13	3.044081e-13

```
dunnTest(m_disease_duration ~ factor(variant, levels = c("LV", "SV", "NF")), data = dat,
  method = "bh")
```

##	Comparison	Z	P.unadj	P.adj
## 1	LV - NF	-0.4419019	6.585602e-01	6.585602e-01
## 2	LV - SV	-4.2131200	2.518672e-05	3.778007e-05
## 3	NF - SV	-4.8097039	1.511540e-06	4.534621e-06

Overall estimates

Estimate the overall effect by fitting an intercept-only model

```
overall <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = dat)
summary(overall, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
## logLik Deviance AIC BIC AICc
## -484.726 969.453 975.453 986.493 975.536
##
## Variance Components:
##
## estim sqrt nlvls fixed factor
## sigma^2.1 0.967 0.984 294 no effectsizeID
## sigma^2.2 0.319 0.565 141 no studyID
##
## Test for Heterogeneity:
## Q(df = 293) = 2585.127, p-val < .001
##
```

```
## Model Results:
##
## estimate      se      tval   df   pval   ci.lb   ci.ub
##   -1.278  0.082  -15.554  293  <.001  -1.439  -1.116  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

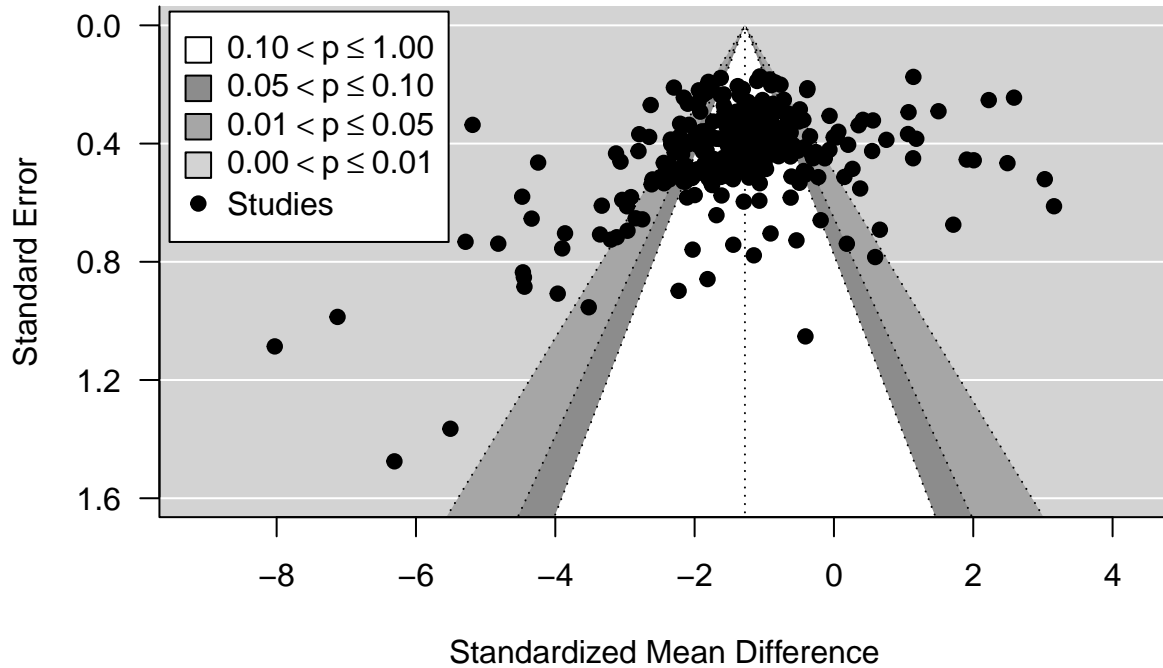
full.model <- rma.mv(yi, vi, random = ~1 | studyID/effectsizeID, tdist = TRUE, data = dat)
summary(full.model, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -484.726  969.453  975.453  986.493  975.536
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed           factor
## sigma^2.1  0.319  0.565   141    no           studyID
## sigma^2.2  0.967  0.984   294    no  studyID/effectsizeID
##
## Test for Heterogeneity:
## Q(df = 293) = 2585.127, p-val < .001
##
## Model Results:
##
## estimate      se      tval   df   pval   ci.lb   ci.ub
##   -1.278  0.082  -15.554  293  <.001  -1.439  -1.116  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Funnel plot

```
funnel.rma(overall, ylim = c(0, 1.6), las = 1, digits = list(1L, 1), level = c(90,
  95, 99), shade = c("white", "gray55", "gray65"), legend = "topleft")
title("Funnel Plot - Common EFs composite")
```

Funnel Plot – Common EFs composite



Rank correlation test

```
ranktest(overall)
```

```
##  
## Rank Correlation Test for Funnel Plot Asymmetry  
##  
## Kendall's tau = -0.1548, p < .0001
```

Heterogeneity of variability

Heterogeneity of within-study variance (level 2)

```
modelnovar2 <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,  
  sigma2 = c(0, NA), data = dat)  
anova(overall, modelnovar2)
```

```
##  
##      df      AIC      BIC      AICc     logLik      LRT     pval      QE
```

```
## Full      3  975.4526  986.4932  975.5357 -484.7263          2585.1267
## Reduced  2 1746.4341 1753.7945 1746.4755 -871.2171  772.9815 <.0001 2585.1267
```

Heterogeneity of between-study variance (level 3)

```
modelnovar3 <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  sigma2 = c(NA, 0), data = dat)
anova(overall, modelnovar3)
```

```
##
##          df      AIC      BIC      AICc    logLik      LRT    pval      QE
## Full      3  975.4526  986.4932  975.5357 -484.7263          2585.1267
## Reduced  2  988.0970  995.4573  988.1383 -492.0485  14.6443  0.0001 2585.1267
```

Distribution of the total variance over the three levels

```
i2 <- var.comp(full.model)
summary(i2)
```

```
##          % of total variance    I2
## Level 1          9.536219    ---
## Level 2         68.026046  68.03
## Level 3         22.437734  22.44
## Total I2: 90.46%
```

Subgroup analysis by executive functions components

Shifting; k = 203; estimate = -1.294, p <.001

```
attach(dat)
shifting <- dat[component == "S", ]
rmashifting <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = shifting)
summary(rmashifting, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -265.089  530.178  536.178  546.103  536.300
##
```

```

## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor
## sigma^2.1 0.399 0.631   203     no  effectsizeID
## sigma^2.2 0.192 0.438   128     no    studyID
##
## Test for Heterogeneity:
## Q(df = 202) = 984.566, p-val < .001
##
## Model Results:
##
## estimate      se      tval   df   pval   ci.lb   ci.ub
##   -1.294  0.068  -19.115  202  <.001  -1.427  -1.160  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Inhibition; $k = 85$; estimate = -1.1723, $p < .001$

```

attach(dat)
inhibition <- dat[component == "I", ]
rmaininhibition <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = inhibition)
summary(rmaininhibition)

```

```

##
## Multivariate Meta-Analysis Model (k = 85; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -168.9348  337.8696  343.8696  351.1620  344.1696
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor
## sigma^2.1 1.3771 1.1735   85     no  effectsizeID
## sigma^2.2 1.9192 1.3853   50     no    studyID
##
## Test for Heterogeneity:
## Q(df = 84) = 1478.2665, p-val < .0001
##
## Model Results:
##
## estimate      se      tval   df   pval   ci.lb   ci.ub
##   -1.1723  0.2477  -4.7334  84  <.0001  -1.6649  -0.6798  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Updating; k = 6; estimate = -0.796, p = 0.0657

```
attach(dat)
updating <- dat[component == "U", ]
rmaupdating <- rma.mv(yi, vi, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = updating)
summary(rmaupdating)
```

```
##
## Multivariate Meta-Analysis Model (k = 6; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -6.0608  12.1216  18.1216  16.9499  42.1216
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0001     6     no  effectsizeID
## sigma^2.2  0.3692  0.6076     5     no     studyID
##
## Test for Heterogeneity:
## Q(df = 5) = 11.8622, p-val = 0.0367
##
## Model Results:
##
## estimate      se      tval  df    pval    ci.lb  ci.ub
## -0.7961  0.3390  -2.3483   5  0.0657  -1.6675  0.0753
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Are the differences between EFs components significant? — p = 0.3459

```
comp.mod <- rma.mv(yi, vi, mods = ~factor(component), random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = dat)
summary(comp.mod)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -481.4168  962.8336  972.8336  991.2002  973.0441
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.9620  0.9808   294     no  effectsizeID
## sigma^2.2  0.3193  0.5651   141     no     studyID
##
## Test for Residual Heterogeneity:
```

```

## QE(df = 291) = 2474.6949, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 291) = 1.0655, p-val = 0.3459
##
## Model Results:
##
##           estimate      se    tval   df    pval   ci.lb   ci.ub
## intrcpt          -1.1346  0.1430  -7.9344 291 <.0001  -1.4160  -0.8532
## factor(component)S -0.2007  0.1576  -1.2734 291  0.2039  -0.5108   0.1095
## factor(component)U  0.2339  0.5180   0.4515 291  0.6519  -0.7856   1.2535
##
## intrcpt          ***
## factor(component)S
## factor(component)U
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Multiple Imputation

```

library(mice)
library(miceadds)

```

Subset dataset

```

datmice <- dat[, c("studyID", "effectsizeID", "study_forestplot", "test", "component",
  "variant", "task_modality", "n1i", "m1i", "sd1i", "n2i", "m2i", "sd2i", "m_disease_duration",
  "m_patient_age", "m_patient_yoe", "yi", "vi")]

```

```

md.pattern(datmice, plot = FALSE)

```

```

##      studyID effectsizeID study_forestplot test component variant task_modality
## 153      1           1           1      1      1           1           1           1
## 91       1           1           1      1      1           1           1           1
## 24       1           1           1      1      1           1           1           1
## 24       1           1           1      1      1           1           1           1
## 2        1           1           1      1      1           1           1           1
##          0           0           0      0      0           0           0           0
##      n1i m1i sd1i n2i m2i sd2i yi vi m_patient_age m_patient_yoe
## 153  1  1  1  1  1  1  1  1  1           1           1
## 91   1  1  1  1  1  1  1  1  1           1           1
## 24   1  1  1  1  1  1  1  1  1           1           0
## 24   1  1  1  1  1  1  1  1  1           1           0
## 2    1  1  1  1  1  1  1  1  1           0           0
##      0  0  0  0  0  0  0  0  0           2           50
##      m_disease_duration
## 153           1  0

```



```
## 91          0  1
## 24          1  1
## 24          0  2
## 2           0  3
##           117 169
```

Proportion of missing data is 40% for disease duration, 0.68% for age of patient and 17% for years of education.

The code -2 in the predictor matrix pred signals that studyID is the cluster variable. The miceadds library is needed for the 2l.pmm method.

```
imp0 <- mice(datmice, maxit = 0)
meth <- imp0$meth
meth[c("m_disease_duration", "m_patient_age", "m_patient_yoe")] <- "2l.pmm"
meth
```

```
##          studyID      effectsizeID  study_forestplot      test
##          ""          ""             ""              ""
##          component      variant      task_modality      n1i
##          ""          ""             ""              ""
##          m1i          sd1i          n2i          m2i
##          ""          ""             ""              ""
##          sd2i m_disease_duration      m_patient_age      m_patient_yoe
##          ""          "2l.pmm"          "2l.pmm"          "2l.pmm"
##          yi          vi
##          ""          ""
```

```
pred <- imp0$pred
pred[, "studyID"] <- -2
pred
```

```
##          studyID effectsizeID study_forestplot test component variant
## studyID          -2          1          0          0          0          0
## effectsizeID      -2          0          0          0          0          0
## study_forestplot -2          1          0          0          0          0
## test              -2          1          0          0          0          0
## component         -2          1          0          0          0          0
## variant           -2          1          0          0          0          0
## task_modality     -2          1          0          0          0          0
## n1i                -2          1          0          0          0          0
## m1i                -2          1          0          0          0          0
## sd1i               -2          1          0          0          0          0
## n2i                -2          1          0          0          0          0
## m2i                -2          1          0          0          0          0
## sd2i              -2          1          0          0          0          0
## m_disease_duration -2          1          0          0          0          0
## m_patient_age      -2          1          0          0          0          0
## m_patient_yoe      -2          1          0          0          0          0
## yi                 -2          1          0          0          0          0
## vi                 -2          1          0          0          0          0
##          task_modality n1i m1i sd1i n2i m2i sd2i m_disease_duration
## studyID          0  1  1  1  1  1  1
## effectsizeID      0  1  1  1  1  1  1
```

```

## study_forestplot      0  1  1  1  1  1  1      1
## test                  0  1  1  1  1  1  1      1
## component             0  1  1  1  1  1  1      1
## variant               0  1  1  1  1  1  1      1
## task_modality        0  1  1  1  1  1  1      1
## n1i                   0  0  1  1  1  1  1      1
## m1i                   0  1  0  1  1  1  1      1
## sd1i                  0  1  1  0  1  1  1      1
## n2i                   0  1  1  1  0  1  1      1
## m2i                   0  1  1  1  1  0  1      1
## sd2i                  0  1  1  1  1  1  0      1
## m_disease_duration    0  1  1  1  1  1  1      0
## m_patient_age         0  1  1  1  1  1  1      1
## m_patient_yoe        0  1  1  1  1  1  1      1
## yi                    0  1  1  1  1  1  1      1
## vi                    0  1  1  1  1  1  1      1
##
##           m_patient_age m_patient_yoe yi vi
## studyID          1             1  1  1
## effectsizeID     1             1  1  1
## study_forestplot 1             1  1  1
## test             1             1  1  1
## component        1             1  1  1
## variant          1             1  1  1
## task_modality    1             1  1  1
## n1i              1             1  1  1
## m1i              1             1  1  1
## sd1i            1             1  1  1
## n2i              1             1  1  1
## m2i              1             1  1  1
## sd2i            1             1  1  1
## m_disease_duration 1             1  1  1
## m_patient_age    0             1  1  1
## m_patient_yoe    1             0  1  1
## yi              1             1  0  1
## vi              1             1  1  0

```

Impute data for the three variables

```

imp <- mice(datmice, m = 10, predictorMatrix = pred, method = meth, print = FALSE,
  seed = 2022)

disease.imp <- with(imp, rma.mv(yi, vi, mods = ~m_disease_duration + m_patient_age +
  m_patient_yoe, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE))

```

Determine correct m by checking the fraction of missing information (fmi)

```
pool(disease.imp)$pooled
```

```
##           term m      estimate      ubar      b      t
## 1      intercept 10  3.959659818 2.2210116313 6.415820e-02 2.2915856482
## 2 m_disease_duration 10  0.059187390 0.0034100126 1.848808e-03 0.0054437011
## 3      m_patient_age 10 -0.083056225 0.0004026465 4.062793e-06 0.0004071156
## 4      m_patient_yoe 10 -0.002028857 0.0011849817 2.144421e-04 0.0014208681
##   dfcom      df      riv      lambda      fmi
## 1    290 271.17294 0.03177562 0.03079702 0.03786704
## 2    290  47.50599 0.59638737 0.37358562 0.39839117
## 3    290 283.77642 0.01109924 0.01097740 0.01787492
## 4    290 138.39923 0.19906329 0.16601567 0.17781183
```

Re-run analysis with $m = 40$

```
imp <- mice(datmice, m = 40, predictorMatrix = pred, method = meth, print = FALSE,
  seed = 2023)
disease.imp <- with(imp, rma.mv(yi, vi, mods = ~m_disease_duration + m_patient_age +
  m_patient_yoe, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE))
summary(pool(disease.imp), conf.int = TRUE)
```

```
##           term      estimate std.error statistic      df      p.value
## 1      intercept  4.103194600 1.56809522  2.6166744 246.84637 9.426882e-03
## 2 m_disease_duration  0.058835137 0.08128351  0.7238262  76.57757 4.713779e-01
## 3      m_patient_age -0.083811202 0.02034899 -4.1186917 279.28430 5.023867e-05
## 4      m_patient_yoe -0.008497678 0.03784737 -0.2245250 192.31603 8.225872e-01
##           2.5 %      97.5 %
## 1  1.01464166  7.19174754
## 2 -0.10303526  0.22070554
## 3 -0.12386807 -0.04375434
## 4 -0.08314691  0.06615155
```

Generate complete() imputed data and refit the model

```
impcomp <- complete(imp)
```

Moderator analysis

Grand mean centering of continuous moderators

```
impcomp$page_cent <- misty::center(impcomp$m_patient_age, type = c("CGM"), cluster = impcomp$effectsizerID,
  value = NULL, as.na = NULL, check = TRUE)
```

```

impcomp$duration_cent <- misty::center(impcomp$m_disease_duration, type = c("CGM"),
  cluster = impcomp$effectsizeID, value = NULL, as.na = NULL, check = TRUE)

```

```

impcomp$yoe_cent <- misty::center(impcomp$m_patient_yoe, type = c("CGM"), cluster = impcomp$effectsizeID,
  value = NULL, as.na = NULL, check = TRUE)

```

PPA (semantic, logopenic and nonfluent variants), LvPPA as intercept, $p < .001$

```

ppa.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV", "NF")),
  random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = impcomp)
summary(ppa.mod.imp)

```

```

##
## Multivariate Meta-Analysis Model (k = 284; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -441.6878  883.3757  893.3757  911.5675  893.5939
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1  0.7836  0.8852   284    no  effectsizeID
## sigma^2.2  0.2611  0.5110   135    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 281) = 2145.5749, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 281) = 28.8801, p-val < .0001
##
## Model Results:
##
##              estimate      se      tval
## intrcpt          -1.9689  0.1732  -11.3669
## factor(variant, levels = c("LV", "SV", "NF"))SV    1.1006  0.1886   5.8364
## factor(variant, levels = c("LV", "SV", "NF"))NF    0.1756  0.1981   0.8863
##
##              df      pval      ci.lb      ci.ub
## intrcpt          281 <.0001  -2.3098  -1.6279
## factor(variant, levels = c("LV", "SV", "NF"))SV    281 <.0001   0.7294   1.4718
## factor(variant, levels = c("LV", "SV", "NF"))NF    281  0.3762  -0.2144   0.5657
##
## intrcpt          ***
## factor(variant, levels = c("LV", "SV", "NF"))SV    ***
## factor(variant, levels = c("LV", "SV", "NF"))NF
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

// LvPPA = -1.9689, SvPPA = -0.8683, NFvPPA = -1.7933 //

```

PPA (semantic, logopenic and nonfluent variants), SvPPA as intercept, $p < .001$

```
ppa.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("SV", "LV", "NF")),
  random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = impcomp)
summary(ppa.mod.imp)
```

```
##
## Multivariate Meta-Analysis Model (k = 284; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -441.6878   883.3757   893.3757   911.5675   893.5939
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor
## sigma^2.1 0.7836 0.8852   284     no  effectsizeID
## sigma^2.2 0.2611 0.5110   135     no     studyID
##
## Test for Residual Heterogeneity:
## QE(df = 281) = 2145.5749, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 281) = 28.8801, p-val < .0001
##
## Model Results:
##
##              estimate      se      tval  df
## intrcpt              -0.8683 0.0938  -9.2544 281
## factor(variant, levels = c("SV", "LV", "NF"))LV -1.1006 0.1886  -5.8364 281
## factor(variant, levels = c("SV", "LV", "NF"))NF -0.9250 0.1435  -6.4463 281
##
##              pval      ci.lb  ci.ub
## intrcpt          <.0001  -1.0530  -0.6836 ***
## factor(variant, levels = c("SV", "LV", "NF"))LV <.0001  -1.4718  -0.7294 ***
## factor(variant, levels = c("SV", "LV", "NF"))NF <.0001  -1.2074  -0.6425 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

PPA (semantic, logopenic and nonfluent variants), NfvPPA as intercept, $p < .001$

```
ppa.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("NF", "SV", "LV")),
  random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = impcomp)
summary(ppa.mod.imp)
```

```
##
## Multivariate Meta-Analysis Model (k = 284; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -441.6878   883.3757   893.3757   911.5675   893.5939
##
```

```

## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.7836 0.8852  284    no  effectsizeID
## sigma^2.2 0.2611 0.5110  135    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 281) = 2145.5749, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 281) = 28.8801, p-val < .0001
##
## Model Results:
##
##              estimate      se      tval
## intrcpt          -1.7933 0.1242 -14.4396
## factor(variant, levels = c("NF", "SV", "LV"))SV  0.9250 0.1435  6.4463
## factor(variant, levels = c("NF", "SV", "LV"))LV -0.1756 0.1981 -0.8863
##
##              df      pval      ci.lb      ci.ub
## intrcpt          281 <.0001 -2.0377 -1.5488
## factor(variant, levels = c("NF", "SV", "LV"))SV  281 <.0001  0.6425  1.2074
## factor(variant, levels = c("NF", "SV", "LV"))LV  281 0.3762 -0.5657  0.2144
##
## intrcpt          ***
## factor(variant, levels = c("NF", "SV", "LV"))SV ***
## factor(variant, levels = c("NF", "SV", "LV"))LV
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Task modality (verbal, nonverbal)

```

task.mod.imp <- rma.mv(yi, vi, mods = ~factor(task_modality), random = list(~1 |
  effectsizeID, ~1 | studyID), tdist = TRUE, data = impcomp)
summary(task.mod.imp)

```

```

##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -483.5141  967.0282  975.0282  989.7353  975.1676
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.9756 0.9877  294    no  effectsizeID
## sigma^2.2 0.3163 0.5624  141    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 292) = 2561.3141, p-val < .0001
##
## Test of Moderators (coefficient 2):

```

```
## F(df1 = 1, df2 = 292) = 0.2239, p-val = 0.6364
##
## Model Results:
##
##           estimate      se      tval  df    pval    ci.lb
## intrcpt          -1.2623  0.0887 -14.2230 292 <.0001 -1.4369
## factor(task_modality)V -0.0799  0.1688  -0.4732 292  0.6364 -0.4122
##           ci.ub
## intrcpt          -1.0876 ***
## factor(task_modality)V  0.2524
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Disease duration

```
disease.mod.imp <- rma.mv(yi, vi, mods = ~duration_cent, random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = impcomp)
summary(disease.mod.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -479.922  959.845   967.845   982.552   967.984
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.921  0.960   294     no  effectsizeID
## sigma^2.2  0.341  0.584   141     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 292) = 2573.289, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 292) = 7.470, p-val = 0.007
##
## Model Results:
##
##           estimate      se      tval  df    pval    ci.lb    ci.ub
## intrcpt          -1.274  0.082 -15.505 292 <.001 -1.436 -1.113 ***
## duration_cent     0.159  0.058  2.733 292  0.007  0.044  0.273 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Age of patient

```
age.mod.imp <- rma.mv(yi, vi, mods = ~age_cent, random = list(~1 | effectsizeID,
~1 | studyID), tdist = TRUE, data = impcomp)
summary(age.mod.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -474.548  949.097  957.097  971.804  957.236
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.879  0.938   294     no  effectsizeID
## sigma^2.2  0.337  0.581   141     no     studyID
##
## Test for Residual Heterogeneity:
## QE(df = 292) = 2446.137, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 292) = 18.586, p-val < .001
##
## Model Results:
##
##           estimate      se      tval  df  pval  ci.lb  ci.ub
## intrcpt      -1.289  0.081  -15.880 292 <.001 -1.449 -1.129 ***
## age_cent     -0.086  0.020   -4.311 292 <.001 -0.125 -0.047 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Years of education

```
yoe.mod.imp <- rma.mv(yi, vi, mods = ~yoe_cent, random = list(~1 | effectsizeID,
~1 | studyID), tdist = TRUE, data = impcomp)
summary(yoe.mod.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 294; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -483.096  966.192  974.192  988.899  974.331
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.970  0.985   294     no  effectsizeID
## sigma^2.2  0.316  0.562   141     no     studyID
##
## Test for Residual Heterogeneity:
```



```

## QE(df = 292) = 2555.039, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 292) = 0.859, p-val = 0.355
##
## Model Results:
##
##           estimate      se      tval   df   pval   ci.lb   ci.ub
## intrcpt      -1.277  0.082 -15.562  292  <.001  -1.438  -1.115  ***
## yoe_cent       0.031  0.033   0.927  292  0.355  -0.035   0.097
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Model with significant moderators

```

sign.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV", "NF")) +
  duration_cent + age_cent, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = impcomp)
summary(sign.mod.imp, digits = 3)

```

```

##
## Multivariate Meta-Analysis Model (k = 284; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -438.911  877.821  891.821  917.240  892.235
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.786  0.887   284    no  effectsizeID
## sigma^2.2  0.269  0.519   135    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 279) = 2134.405, p-val < .001
##
## Test of Moderators (coefficients 2:5):
## F(df1 = 4, df2 = 279) = 14.634, p-val < .001
##
## Model Results:
##
##           estimate      se      tval   df
## intrcpt      -1.942  0.177 -10.951  279
## factor(variant, levels = c("LV", "SV", "NF"))SV   1.030  0.204   5.048  279
## factor(variant, levels = c("LV", "SV", "NF"))NF   0.205  0.200   1.021  279
## duration_cent   0.020  0.059   0.336  279
## age_cent      -0.022  0.022  -1.024  279
##
##           pval   ci.lb   ci.ub
## intrcpt      <.001  -2.291  -1.593  ***
## factor(variant, levels = c("LV", "SV", "NF"))SV <.001   0.629   1.432  ***
## factor(variant, levels = c("LV", "SV", "NF"))NF 0.308  -0.190   0.599
## duration_cent 0.737  -0.097   0.136

```

```
## age_cent                0.307  -0.065  0.021
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Heterogeneity of variability after moderator analysis

Heterogeneity of within-study variance (level 2)

```
modelnovar2.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("NF", "SV",
  "LV"))) + duration_cent + age_cent, random = list(~1 | effectsizeID, ~1 | studyID),
  tdist = TRUE, sigma2 = c(0, NA), data = impcomp)
anova(sign.mod.imp, modelnovar2.mod.imp)
```

```
##
##          df          AIC          BIC          AICc          logLik          LRT          pval          QE
## Full      7  891.8214  917.2399  892.2347 -438.9107                2134.4048
## Reduced   6 1553.3217 1575.1090 1553.6306 -770.6609 663.5003 <.0001 2134.4048
```

Heterogeneity of between-study variance (level 3)

```
modelnovar3.mod.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("NF", "SV",
  "LV"))) + duration_cent + age_cent, random = list(~1 | effectsizeID, ~1 | studyID),
  tdist = TRUE, sigma2 = c(NA, 0), data = impcomp)
anova(sign.mod.imp, modelnovar3.mod.imp)
```

```
##
##          df          AIC          BIC          AICc          logLik          LRT          pval          QE
## Full      7  891.8214  917.2399  892.2347 -438.9107                2134.4048
## Reduced   6  906.6490  928.4363  906.9579 -447.3245 16.8276 <.0001 2134.4048
```

Subset the data by executive functions components after imputation

Shifting — k = 203, est = -1.294

```
attach(impcomp)
shifting.imp <- impcomp[component == "S", ]
```

Inhibition — k = 85, est = -1.1723

```
inhibition.imp <- impcomp[component == "I", ]
```

Updating — k = 6, est = -0.7961

```
updating.imp <- impcomp[component == "U", ]
```

Moderator analysis in the three groups of executive functions

Shifting

Grand mean centering of continuous moderators within shifting

```
shifting.imp$page_cent <- misty::center(shifting.imp$m_patient_age, type = c("CGM"),  
  cluster = shifting$effectsizeID, value = NULL, as.na = NULL, check = TRUE)
```

```
shifting.imp$duration_cent <- misty::center(shifting.imp$m_disease_duration, type = c("CGM"),  
  cluster = shifting$effectsizeID, value = NULL, as.na = NULL, check = TRUE)
```

```
shifting.imp$yoe_cent <- misty::center(shifting.imp$m_patient_yoe, type = c("CGM"),  
  cluster = shifting.imp$effectsizeID, value = NULL, as.na = NULL, check = TRUE)
```

PPA (semantic, logopenic and nonfluent variants), LvPPA as intercept, $p < 0.0001$

```
ppa.mod.shift.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV",  
  "NF")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = shifting.imp)  
summary(ppa.mod.shift.imp, digits = 3)
```

```
##  
## Multivariate Meta-Analysis Model (k = 197; method: REML)  
##  
##   logLik  Deviance      AIC      BIC      AICc  
## -211.662  423.323  433.323  449.663  433.643  
##  
## Variance Components:  
##  
##           estim  sqrt  nlvls  fixed      factor  
## sigma^2.1  0.146  0.383   197    no  effectsizeID  
## sigma^2.2  0.174  0.417   123    no    studyID  
##  
## Test for Residual Heterogeneity:  
## QE(df = 194) = 585.572, p-val < .001  
##  
## Test of Moderators (coefficients 2:3):
```

```
## F(df1 = 2, df2 = 194) = 52.757, p-val < .001
##
## Model Results:
##
##               estimate      se      tval  df
## intrcpt          -2.074  0.118 -17.571 194
## factor(variant, levels = c("LV", "SV", "NF"))SV    1.171  0.127   9.190 194
## factor(variant, levels = c("LV", "SV", "NF"))NF    0.460  0.133   3.451 194
##               pval    ci.lb    ci.ub
## intrcpt          <.001 -2.307 -1.841 ***
## factor(variant, levels = c("LV", "SV", "NF"))SV <.001  0.920  1.422 ***
## factor(variant, levels = c("LV", "SV", "NF"))NF <.001  0.197  0.723 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
// LvPPA = -2.0739, NFvPPA = -1.6141, SvPPA = - 0.9689 //
```

PPA (semantic, logopenic and nonfluent variants), SvPPA as intercept, p <0.0001

```
ppa.mod.shift.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("SV", "LV",
  "NF")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = shifting.imp)
summary(ppa.mod.shift.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 197; method: REML)
##
##   logLik Deviance      AIC      BIC      AICc
## -211.662  423.323  433.323  449.663  433.643
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.146  0.383   197    no  effectsizeID
## sigma^2.2  0.174  0.417   123    no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 194) = 585.572, p-val < .001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 194) = 52.757, p-val < .001
##
## Model Results:
##
##               estimate      se      tval  df
## intrcpt          -0.903  0.068 -13.254 194
## factor(variant, levels = c("SV", "LV", "NF"))LV    -1.171  0.127   -9.190 194
## factor(variant, levels = c("SV", "LV", "NF"))NF    -0.711  0.097   -7.300 194
##               pval    ci.lb    ci.ub
## intrcpt          <.001 -1.037 -0.768 ***
## factor(variant, levels = c("SV", "LV", "NF"))LV <.001 -1.422 -0.920 ***
## factor(variant, levels = c("SV", "LV", "NF"))NF <.001 -0.904 -0.519 ***
```

```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

PPA (semantic, logopenic and nonfluent variants), NfvPPA as intercept, $p < 0.0001$

```
ppa.mod.shift.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("NF", "LV",
  "SV")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = shifting.imp)
summary(ppa.mod.shift.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 197; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -211.662  423.323  433.323  449.663  433.643
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.146  0.383   197     no  effectsizeID
## sigma^2.2  0.174  0.417   123     no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 194) = 585.572, p-val < .001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 194) = 52.757, p-val < .001
##
## Model Results:
##
##                                     estimate      se      tval  df
## intrcpt                             -1.614  0.088  -18.444  194
## factor(variant, levels = c("NF", "LV", "SV"))LV  -0.460  0.133  -3.451  194
## factor(variant, levels = c("NF", "LV", "SV"))SV   0.711  0.097   7.300  194
##
##                                     pval  ci.lb  ci.ub
## intrcpt                             <.001  -1.787  -1.441  ***
## factor(variant, levels = c("NF", "LV", "SV"))LV  <.001  -0.723  -0.197  ***
## factor(variant, levels = c("NF", "LV", "SV"))SV  <.001   0.519   0.904  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Task modality (verbal, nonverbal) not applicable under shifting

Disease duration

```
disease.mod.shift.imp <- rma.mv(yi, vi, mods = ~duration_cent, random = list(~1 |
  effectsizeID, ~1 | studyID), tdist = TRUE, data = shifting.imp)
summary(disease.mod.shift.imp, digit = 3)
```

```

##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -261.530  523.060   531.060   544.273   531.264
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.381  0.617   203     no  effectsizeID
## sigma^2.2  0.191  0.437   128     no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 944.623, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 201) = 5.626, p-val = 0.019
##
## Model Results:
##
##           estimate      se      tval   df   pval   ci.lb   ci.ub   ***
## intrcpt          -1.290  0.067  -19.279  201 <.001  -1.422  -1.158   ***
## duration_cent     0.116  0.049   2.372  201  0.019   0.020   0.212    *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Age of patient

```

age.mod.shift.imp <- rma.mv(yi, vi, mods = ~age_cent, random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = shifting.imp)
summary(age.mod.shift.imp, digits = 3)

```

```

##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -249.831  499.663   507.663   520.876   507.867
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.296  0.544   203     no  effectsizeID
## sigma^2.2  0.207  0.455   128     no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 866.209, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 201) = 31.213, p-val < .001
##
## Model Results:

```

```
##
##          estimate      se      tval   df   pval   ci.lb   ci.ub
## intrcpt      -1.289  0.065  -19.949  201  <.001  -1.416  -1.162  ***
## age_cent     -0.090  0.016   -5.587  201  <.001  -0.122  -0.058  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Years of education

```
yoe.mod.shift.imp <- rma.mv(yi, vi, mods = ~yoe_cent, random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = shifting.imp)
summary(yoe.mod.shift.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -263.964  527.929  535.929  549.142  536.133
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.401  0.633   203     no  effectsizeID
## sigma^2.2  0.192  0.439   128     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 983.257, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 201) = 0.548, p-val = 0.460
##
## Model Results:
##
##           estimate      se      tval   df   pval   ci.lb   ci.ub
## intrcpt      -1.293  0.068  -19.080  201  <.001  -1.427  -1.159  ***
## yoe_cent       0.020  0.027   0.741  201  0.460  -0.034  0.074
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model with significant moderators

```
sign.mod.shift.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV",
  "NF")) + duration_cent + age_cent, random = list(~1 | effectsizeID, ~1 | studyID),
  tdist = TRUE, data = shifting.imp)
summary(sign.mod.shift.imp, digits = 3)
```

```
##
```

```

## Multivariate Meta-Analysis Model (k = 197; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -207.628  415.256  429.256  452.059  429.865
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  0.141  0.375   197     no  effectsizeID
## sigma^2.2  0.180  0.425   123     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 192) = 581.833, p-val < .001
##
## Test of Moderators (coefficients 2:5):
## F(df1 = 4, df2 = 192) = 28.026, p-val < .001
##
## Model Results:
##
##                                     estimate      se      tval  df
## intrcpt                               -2.072  0.121  -17.098  192
## factor(variant, levels = c("LV", "SV", "NF"))SV    1.127  0.139   8.099  192
## factor(variant, levels = c("LV", "SV", "NF"))NF    0.530  0.136   3.902  192
## duration_cent                                -0.038  0.044  -0.874  192
## age_cent                                    -0.037  0.017  -2.203  192
##
##                                     pval  ci.lb  ci.ub
## intrcpt                               <.001  -2.311  -1.833  ***
## factor(variant, levels = c("LV", "SV", "NF"))SV <.001   0.853   1.402  ***
## factor(variant, levels = c("LV", "SV", "NF"))NF <.001   0.262   0.798  ***
## duration_cent                                0.383  -0.124   0.048
## age_cent                                    0.029  -0.070  -0.004  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Inhibition

Grand mean centering of continuous moderators within inhibition

```

inhibition.imp$age_cent <- misty::center(inhibition.imp$m_patient_age, type = c("CGM"),
  cluster = inhibition.imp$effectsizeID, value = NULL, as.na = NULL, check = TRUE)

```

```

inhibition.imp$duration_cent <- misty::center(inhibition.imp$m_disease_duration,
  type = c("CGM"), cluster = inhibition.imp$effectsizeID, value = NULL, as.na = NULL,
  check = TRUE)

```

```

inhibition.imp$yoe_cent <- misty::center(inhibition.imp$m_patient_yoe, type = c("CGM"),
  cluster = inhibition.imp$effectsizeID, value = NULL, as.na = NULL, check = TRUE)

```


PPA (semantic, logopenic and nonfluent variants), LvPPA as intercept, $p = 0.0002$

```
ppa.mod.inhib.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV",
  "NF")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(ppa.mod.inhib.imp)
```

```
##
## Multivariate Meta-Analysis Model (k = 81; method: REML)
##
##   logLik   Deviance      AIC      BIC      AICc
## -151.8077  303.6155  313.6155  325.3990  314.4488
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor
## sigma^2.1  1.1192  1.0579    81    no  effectsizeID
## sigma^2.2  1.8025  1.3426    48    no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 78) = 1379.6351, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 78) = 9.3991, p-val = 0.0002
##
## Model Results:
##
##                                     estimate      se      tval  df
## intrcpt                             -1.3906  0.5172  -2.6887  78
## factor(variant, levels = c("LV", "SV", "NF"))SV  0.6502  0.5103  1.2742  78
## factor(variant, levels = c("LV", "SV", "NF"))NF -0.8204  0.5118  -1.6029  78
##
##                                     pval      ci.lb      ci.ub
## intrcpt                             0.0088  -2.4203  -0.3609  **
## factor(variant, levels = c("LV", "SV", "NF"))SV 0.2064  -0.3657  1.6662
## factor(variant, levels = c("LV", "SV", "NF"))NF 0.1130  -1.8394  0.1986
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
// LvPPA = -1.3906, SvPPA = -0.7404, NFvPPA = -2.2110 //
```

PPA (semantic, logopenic and nonfluent variants), SvPPA as intercept, $p = 0.0002$

```
ppa.mod.inhib.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("SV", "NF",
  "LV")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(ppa.mod.inhib.imp)
```

```
##
## Multivariate Meta-Analysis Model (k = 81; method: REML)
##
##   logLik   Deviance      AIC      BIC      AICc
```

```

## -151.8077  303.6155  313.6155  325.3990  314.4488
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.1192  1.0579    81    no  effectsizeID
## sigma^2.2  1.8025  1.3426    48    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 78) = 1379.6351, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 78) = 9.3991, p-val = 0.0002
##
## Model Results:
##
##                                estimate      se      tval  df
## intrcpt                        -0.7404  0.2614  -2.8326  78
## factor(variant, levels = c("SV", "NF", "LV"))NF -1.4706  0.3394  -4.3329  78
## factor(variant, levels = c("SV", "NF", "LV"))LV  -0.6502  0.5103  -1.2742  78
##                                pval      ci.lb      ci.ub
## intrcpt                        0.0059  -1.2607  -0.2200  **
## factor(variant, levels = c("SV", "NF", "LV"))NF <.0001  -2.1463  -0.7949  ***
## factor(variant, levels = c("SV", "NF", "LV"))LV  0.2064  -1.6662   0.3657
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

PPA (semantic, logopenic and nonfluent variants), NfvPPA as intercept, $p = 0.0002$

```

ppa.mod.inhib.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("NF", "SV",
  "LV")), random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(ppa.mod.inhib.imp)

```

```

##
## Multivariate Meta-Analysis Model (k = 81; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -151.8077  303.6155  313.6155  325.3990  314.4488
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.1192  1.0579    81    no  effectsizeID
## sigma^2.2  1.8025  1.3426    48    no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 78) = 1379.6351, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 78) = 9.3991, p-val = 0.0002
##

```

```
## Model Results:
##
##
##          estimate      se    tval  df
## intrcpt          -2.2110  0.3427  -6.4521  78
## factor(variant, levels = c("NF", "SV", "LV"))SV    1.4706  0.3394   4.3329  78
## factor(variant, levels = c("NF", "SV", "LV"))LV    0.8204  0.5118   1.6029  78
##
##          pval    ci.lb    ci.ub
## intrcpt    <.0001  -2.8932  -1.5288  ***
## factor(variant, levels = c("NF", "SV", "LV"))SV <.0001   0.7949   2.1463  ***
## factor(variant, levels = c("NF", "SV", "LV"))LV  0.1130  -0.1986   1.8394
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Task modality (verbal, nonverbal)

```
task.mod.inhib.imp <- rma.mv(yi, vi, mods = ~factor(task_modality), random = list(~1 |
  effectsizeID, ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(task.mod.inhib.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 85; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -166.361  332.721  340.721  350.397  341.234
##
## Variance Components:
##
##          estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.382  1.176    85     no  effectsizeID
## sigma^2.2  1.829  1.352    50     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 83) = 1454.048, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 83) = 2.206, p-val = 0.141
##
## Model Results:
##
##          estimate      se    tval  df  pval    ci.lb    ci.ub
## intrcpt          -0.674  0.416  -1.620  83  0.109  -1.500  0.153
## factor(task_modality)V    -0.637  0.429  -1.485  83  0.141  -1.490  0.216
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Disease duration

```
disease.mod.inhib.imp <- rma.mv(yi, vi, mods = ~duration_cent, random = list(~1 |
  effectsizeID, ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(disease.mod.inhib.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 85; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -165.361  330.722  338.722  348.397  339.234
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.172  1.082    85     no  effectsizeID
## sigma^2.2  2.101  1.449    50     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 83) = 1463.310, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 83) = 4.660, p-val = 0.034
##
## Model Results:
##
##           estimate      se    tval  df  pval  ci.lb  ci.ub
## intrcpt          -1.178  0.250  -4.721  83  <.001  -1.675  -0.682 ***
## duration_cent     0.307  0.142   2.159  83  0.034   0.024   0.591  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Age of patient

```
age.mod.inhib.imp <- rma.mv(yi, vi, mods = ~age_cent, random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(age.mod.inhib.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 85; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -165.894  331.789  339.789  349.464  340.301
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.224  1.106    85     no  effectsizeID
## sigma^2.2  2.103  1.450    50     no    studyID
##
## Test for Residual Heterogeneity:
```

```

## QE(df = 83) = 1418.582, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 83) = 3.282, p-val = 0.074
##
## Model Results:
##
##           estimate      se    tval  df  pval  ci.lb  ci.ub
## intrcpt      -1.207  0.252  -4.785  83  <.001  -1.708  -0.705  ***
## age_cent     -0.093  0.051  -1.812  83  0.074  -0.196   0.009
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Years of education

```

yoe.mod.inhib.imp <- rma.mv(yi, vi, mods = ~yoe_cent, random = list(~1 | effectsizeID,
  ~1 | studyID), tdist = TRUE, data = inhibition.imp)
summary(yoe.mod.inhib.imp, digits = 3)

```

```

##
## Multivariate Meta-Analysis Model (k = 85; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -167.367  334.735  342.735  352.410  343.247
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.402  1.184    85     no  effectsizeID
## sigma^2.2  1.943  1.394    50     no    studyID
##
## Test for Residual Heterogeneity:
## QE(df = 83) = 1403.915, p-val < .001
##
## Test of Moderators (coefficient 2):
## F(df1 = 1, df2 = 83) = 0.000, p-val = 0.989
##
## Model Results:
##
##           estimate      se    tval  df  pval  ci.lb  ci.ub
## intrcpt      -1.173  0.250  -4.701  83  <.001  -1.670  -0.677  ***
## yoe_cent       0.001  0.104   0.013  83  0.989  -0.205   0.208
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Model with significant moderators

```
sign.mod.inhib.imp <- rma.mv(yi, vi, mods = ~factor(variant, levels = c("LV", "SV",
  "NF")) + duration_cent, random = list(~1 | effectsizeID, ~1 | studyID), tdist = TRUE,
  data = inhibition.imp)
summary(sign.mod.inhib.imp, digits = 3)
```

```
##
## Multivariate Meta-Analysis Model (k = 81; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -150.270  300.541  312.541  326.603  313.741
##
## Variance Components:
##
##           estim  sqrt  nlvls  fixed      factor
## sigma^2.1  1.113  1.055     81     no  effectsizeID
## sigma^2.2  1.852  1.361     48     no      studyID
##
## Test for Residual Heterogeneity:
## QE(df = 77) = 1347.835, p-val < .001
##
## Test of Moderators (coefficients 2:4):
## F(df1 = 3, df2 = 77) = 6.340, p-val < .001
##
## Model Results:
##
##                                     estimate    se    tval  df
## intrcpt                               -1.369  0.520  -2.634  77
## factor(variant, levels = c("LV", "SV", "NF"))SV    0.596  0.521   1.143  77
## factor(variant, levels = c("LV", "SV", "NF"))NF   -0.792  0.513  -1.545  77
## duration_cent                                0.080  0.153   0.526  77
##
##                                     pval    ci.lb  ci.ub
## intrcpt                                0.010  -2.404  -0.334  *
## factor(variant, levels = c("LV", "SV", "NF"))SV  0.257  -0.442   1.634
## factor(variant, levels = c("LV", "SV", "NF"))NF  0.126  -1.813   0.229
## duration_cent                                0.600  -0.224   0.385
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

•